

# SEQUENCE LISTING

<110> The Government of the United States of America, as

<120> MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND  
SIV ENV GENES

<130> 2026-4287US1 HIV GAG/POL, SIV GAG & ENV

<140> TO BE ASSIGNED

<141> 2001-06-01

<150> PCT/US00/34985

<151> 2000-12-22

<150> 60/173,036

<151> 1999-12-23

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 4338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated Human  
Immunodeficiency Virus - 1 Gag/Pol gene

<400> 1

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<210> 2

<211> 2507

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 2

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<210> 3

<211> 2467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated Human  
Immunodeficiency Virus - 1 Pol gene

<400> 3

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<210> 4

<211> 1533

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Mutated  
Simian Immunodeficiency Virus Gag gene

<400> 4

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<210> 5

<211> 1532

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence of mutated Simian Immunodeficiency Virus  
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gene

<400> 5

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<210> 6  
 <211> 8366  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
 of the construct pCMVgagpolBNKan containing a CMV  
 promoter, a HIV gag/pol gene and a kanamycin  
 resistance gene

<400> 6

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<210> 10

<211> 122

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
 of the BSSHII to ClaI fragment in transfer  
 construct pmBCwCNluci and pmBCmCNluci

<400> 10

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 cg 122

<210> 11

<211> 122

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
 of the BSSHII to ClaI fragment in transfer  
 construct 3

<400> 11

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 cg 122

<210> 12

<211> 122

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 12

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 cg 122

<210> 13  
<211> 122  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Plurality  
Consensus sequence of DNA sequence of the BSSHII  
to CLaI fragment in HIV-1 and transfer constructs

<400> 13  
cgcgacacggc aagagggcgag gggcgggcgac tggtagtagtac gccaaaaatt ttgactagcg 60  
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aa 122

<210> 14  
<211> 122  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: DNA sequence  
of construct CMVkan/R-R-SIVgp160 CTE

<400> 14  
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cg 122

<210> 15  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: DNA sequence  
of construct CMVkan/R-R-SIVgp160 CTE

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<210> 16

<211> 879

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SIV gp160env  
IN PLASMID CMVkan/R-R-SIVgp160 CTE

<400> 16

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Met Gly Cys Leu Gly Asn Gln Leu Leu Ile Ala Ile Leu Leu Leu Ser
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```

```

Val Tyr Gly Ile Tyr Cys Thr Leu Tyr Val Thr Val Phe Tyr Gly Val
      20              25              30

```

```

Pro Ala Trp Arg Asn Ala Thr Ile Pro Leu Phe Cys Ala Thr Lys Asn
      35              40              45

```

```

Arg Asp Thr Trp Gly Thr Thr Gln Cys Leu Pro Asp Asn Gly Asp Tyr
      50              55              60

```

```

Ser Glu Val Ala Leu Asn Val Thr Glu Ser Phe Asp Ala Trp Asn Asn
      65              70              75              80

```

```

Thr Val Thr Glu Gln Ala Ile Glu Asp Val Trp Gln Leu Phe Glu Thr
      85              90              95

```

```

Ser Ile Lys Pro Cys Val Lys Leu Ser Pro Leu Cys Ile Thr Met Arg
      100             105             110

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Cys Asn Lys Ser Glu Thr Asp Arg Trp Gly Leu Thr Lys Ser Ile Thr  
115 120 125

Thr Thr Ala Ser Thr Thr Ser Thr Thr Ala Ser Ala Lys Val Asp Met  
130 135 140

Val Asn Glu Thr Ser Ser Cys Ile Ala Gln Asp Asn Cys Thr Gly Leu  
145 150 155 160

Glu Gln Glu Gln Met Ile Ser Cys Lys Phe Asn Met Thr Gly Leu Lys  
165 170 175

Arg Asp Lys Lys Lys Glu Tyr Asn Glu Thr Trp Tyr Ser Ala Asp Leu  
180 185 190

Val Cys Glu Gln Gly Asn Asn Thr Gly Asn Glu Ser Arg Cys Tyr Met  
195 200 205

Asn His Cys Asn Thr Ser Val Ile Gln Glu Ser Cys Asp Lys His Tyr  
210 215 220

Trp Asp Ala Ile Arg Phe Arg Tyr Cys Ala Pro Pro Gly Tyr Ala Leu  
225 230 235 240

Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Met Pro Lys Cys Ser  
245 250 255

Lys Val Val Val Ser Ser Cys Thr Arg Met Met Glu Thr Gln Thr Ser  
260 265 270

Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile  
275 280 285

Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser Leu Asn Lys Tyr  
290 295 300

Tyr Asn Leu Thr Met Lys Cys Arg Arg Pro Gly Asn Lys Thr Val Leu  
305 310 315 320

Pro Val Thr Ile Met Ser Gly Leu Val Phe His Ser Gln Pro Ile Asn  
325 330 335

Asp Arg Pro Lys Gln Ala Trp Cys Trp Phe Gly Gly Lys Trp Lys Asp  
340 345 350

Ala Ile Lys Glu Val Lys Gln Thr Ile Val Lys His Pro Arg Tyr Thr  
355 360 365

Gly Thr Asn Asn Thr Asp Lys Ile Asn Leu Thr Ala Pro Gly Gly Gly  
 370 375 380

Asp Pro Glu Val Thr Phe Met Trp Thr Asn Cys Arg Gly Glu Phe Leu  
 385 390 395 400

Tyr Cys Lys Met Asn Trp Phe Leu Asn Trp Val Glu Asp Arg Asn Thr  
 405 410 415

Ala Asn Gln Lys Pro Lys Glu Gln His Lys Arg Asn Tyr Val Pro Cys  
 420 425 430

His Ile Arg Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys Asn Val  
 435 440 445

Tyr Leu Pro Pro Arg Glu Gly Asp Leu Thr Cys Asn Ser Thr Val Thr  
 450 455 460

Ser Leu Ile Ala Asn Ile Asp Trp Ile Asp Gly Asn Gln Thr Asn Ile  
 465 470 475 480

Thr Met Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp  
 485 490 495

Tyr Lys Leu Val Glu Ile Thr Pro Ile Gly Leu Ala Pro Thr Asp Val  
 500 505 510

Lys Arg Tyr Thr Thr Gly Gly Thr Ser Arg Asn Lys Arg Gly Val Phe  
 515 520 525

Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly  
 530 535 540

Ala Ala Ser Leu Thr Leu Thr Ala Gln Ser Arg Thr Leu Leu Ala Gly  
 545 550 555 560

Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln  
 565 570 575

Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Thr Arg  
 580 585 590

Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ala  
 595 600 605

Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Pro  
 610 615 620





```
<400> 17
Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn
  1             5             10             15
```

Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp  
35 40 45

Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro  
65 70 75 80

Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu  
100 105 110

Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp  
130 135 140

Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu  
165 170 175

Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu  
195 200 205

26

210	215	220
Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser		
225	230	235 240
Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro		
245	250	255
Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe		
260	265	270

<210> 18  
 <211> 2640  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DNA sequence  
 of mutated SIV gene in construct  
 CMVkan/R-R-SIVgp160 CTE

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